

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/749,522

Source: _____

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/749,522

DATE: 01/13/2005

TIME: 12:17:14

Input Set : N:\Crf3\RULE60\10749522.raw.txt
 Output Set: N:\CRF4\01132005\J749522.raw

1 <110> APPLICANT: SOLOMON, Beka
 2 HANAN, Eilat
 3 <120> TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME USEFUL IN
 DIAGNOSING
 4 AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES
 5 <130> FILE REFERENCE: SOLOMON=2B
 6 <140> CURRENT APPLICATION NUMBER: US/10/749,522
 7 <141> CURRENT FILING DATE: 2004-01-02
 8 <150> PRIOR APPLICATION NUMBER: US/09/629,971
 9 <151> PRIOR FILING DATE: 2000-07-31
 10 <150> PRIOR APPLICATION NUMBER: US 09/473,653
 11 <151> PRIOR FILING DATE: 1999-12-29
 12 <150> PRIOR APPLICATION NUMBER: US 60/152,417
 13 <151> PRIOR FILING DATE: 1999-09-03
 14 <160> NUMBER OF SEQ ID NOS: 29
 15 <170> SOFTWARE: PatentIn version 3.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 4
 19 <212> TYPE: PRT
 20 <213> ORGANISM: Artificial
 21 <220> FEATURE:
 22 <223> OTHER INFORMATION: synthetic peptide
 23 <400> SEQUENCE: 1
 24 Glu Phe Arg His
 25 1
 27 <210> SEQ ID NO: 2
 28 <211> LENGTH: 15
 29 <212> TYPE: PRT
 30 <213> ORGANISM: Artificial
 31 <220> FEATURE:
 32 <223> OTHER INFORMATION: synthetic peptide
 33 <400> SEQUENCE: 2
 34 Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 35 1 5 10 15
 37 <210> SEQ ID NO: 3
 38 <211> LENGTH: 43
 39 <212> TYPE: PRT
 40 <213> ORGANISM: Artificial
 41 <220> FEATURE:
 42 <223> OTHER INFORMATION: synthetic peptide
 43 <400> SEQUENCE: 3
 44 Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
 45 1 5 10 15
 46 Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile

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47          20          25          30
48      Gly Leu Met Val Gly Gly Val Val Ile Ala Thr
49          35          40
51 <210> SEQ ID NO: 4
52 <211> LENGTH: 4
53 <212> TYPE: PRT
54 <213> ORGANISM: Artificial
55 <220> FEATURE:
56 <223> OTHER INFORMATION: synthetic peptide
57 <400> SEQUENCE: 4
58     Trp Val Leu Asp
59     1
61 <210> SEQ ID NO: 5
62 <211> LENGTH: 717
63 <212> TYPE: DNA
64 <213> ORGANISM: Homo sapiens
65 <220> FEATURE:
66 <221> NAME/KEY: CDS
67 <222> LOCATION: (1)..(717)
68 <400> SEQUENCE: 5
69     cag gtc aaa ctg cag gag tca ggg gct gag ctg gtg agg cct ggg gtc          48
70     Gln Val Lys Leu Gln Glu Ser Gly Ala Glu Leu Val Arg Pro Gly Val
71     1          5          10          15
72     tca gtg aag att tcc tgc aag ggt tct ggc tac aca ttc act gat tat          96
73     Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
74     20          25          30
75     gct atg cac tgg gtg aag cag agt cat gca aag agt cta gag tgg att          144
76     Ala Met His Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile
77     35          40          45
78     gga gtt att agt act tac tat ggt gat gct agc tac aac cag aag ttc          192
79     Gly Val Ile Ser Thr Tyr Tyr Gly Asp Ala Ser Tyr Asn Gln Lys Phe
80     50          55          60
81     aag ggc aag gcc aca atg act gta gac aaa tcc tcc agc aca gcc tat          240
82     Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
83     65          70          75          80
84     atg gaa ctt gcc aga ctg aca tct gag gat tct gcc atc tat tac tgt          288
85     Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
86     85          90          95
87     gca aga ggg gct act atg tcc tac ttt gac tac tgg ggc caa gtg acc          336
88     Ala Arg Gly Ala Thr Met Ser Tyr Phe Asp Tyr Trp Gly Gln Val Thr
89     100         105         110
90     acg gtc acc gtc tcc tca ggt gga ggc ggt tca ggc gga gtt ggc tct          384
91     Thr Val Thr Val Ser Ser Gly Gly Ser Gly Gly Val Gly Ser
92     115         120         125
93     ggc ggt ggc gga tcg gac atc gag ctc act cag tct cca gca atc atg          432
94     Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met
95     130         135         140
96     tct gca tct cca ggg gag aag gtc acc atg acc tgc agt gcc agc tca          480
97     Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser

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98	145	150	155	160	
99	agt ata agt tac atg cac tgg tat cag cag aag cca ggc acc tcc ccc				528
100	Ser Ile Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Thr Ser Pro				
101	165	170	175		
102	aaa aga tgg att tat gac aca tcc aaa ctg gct tct gga gtc cct gct				576
103	Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala				
104	180	185	190		
105	cgc ttc agt ggc agt ggg tct ggg acc tct tat tct ctc aca atc agc				624
106	Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser				
107	195	200	205		
108	agc atg gag gct gaa gat gct gcc act tat tac tgc cat cag cgg agt				672
109	Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser				
110	210	215	220		
111	agt tac cca ttc acg ttc gga ggg ggg gcc aag ctg gaa ata aaa				717
112	Ser Tyr Pro Phe Thr Phe Gly Gly Ala Lys Leu Glu Ile Lys				
113	225	230	235		
115	<210> SEQ ID NO: 6				
116	<211> LENGTH: 239				
117	<212> TYPE: PRT				
118	<213> ORGANISM: Homo sapiens				
119	<400> SEQUENCE: 6				
120	Gln Val Lys Leu Gln Glu Ser Gly Ala Glu Leu Val Arg Pro Gly Val				
121	1	5	10	15	
122	Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr				
123	20	25	30		
124	Ala Met His Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile				
125	35	40	45		
126	Gly Val Ile Ser Thr Tyr Tyr Gly Asp Ala Ser Tyr Asn Gln Lys Phe				
127	50	55	60		
128	Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr				
129	65	70	75	80	
130	Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys				
131	85	90	95		
132	Ala Arg Gly Ala Thr Met Ser Tyr Phe Asp Tyr Trp Gly Gln Val Thr				
133	100	105	110		
134	Thr Val Thr Val Ser Ser Gly Gly Ser Gly Gly Val Gly Ser				
135	115	120	125		
136	Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met				
137	130	135	140		
138	Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser				
139	145	150	155	160	
140	Ser Ile Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Thr Ser Pro				
141	165	170	175		
142	Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala				
143	180	185	190		
144	Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser				
145	195	200	205		
146	Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser				
147	210	215	220		

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148      Ser Tyr Pro Phe Thr Phe Gly Gly Ala Lys Leu Glu Ile Lys
149      225          230          235
151 <210> SEQ ID NO: 7
152 <211> LENGTH: 6
153 <212> TYPE: PRT
154 <213> ORGANISM: Artificial
155 <220> FEATURE:
156 <223> OTHER INFORMATION: synthetic peptide
157 <400> SEQUENCE: 7
158      Tyr Tyr Glu Phe Arg His
159      1           5
161 <210> SEQ ID NO: 8
162 <211> LENGTH: 15
163 <212> TYPE: PRT
164 <213> ORGANISM: Artificial
165 <220> FEATURE:
166 <223> OTHER INFORMATION: synthetic peptide
167 <400> SEQUENCE: 8
168      Val His Glu Pro His Glu Phe Arg His Val Ala Leu Asn Pro Val
169      1           5           10          15
171 <210> SEQ ID NO: 9
172 <211> LENGTH: 3
173 <212> TYPE: PRT
174 <213> ORGANISM: Artificial
175 <220> FEATURE:
176 <223> OTHER INFORMATION: synthetic peptide
177 <400> SEQUENCE: 9
178      Lys Leu His
179      1
181 <210> SEQ ID NO: 10
182 <211> LENGTH: 45
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial
185 <220> FEATURE:
186 <223> OTHER INFORMATION: primer
W--> 187 <221> NAME/KEY: misc_feature
188 <223> OTHER INFORMATION: "n" at position 17 is unknown
W--> 189 <400> 10
W--> 190      ccccccctccg aacgttsnatg ggtaactcga tcgctgatgg cagta      45
192 <210> SEQ ID NO: 11
193 <211> LENGTH: 24
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial
196 <220> FEATURE:
197 <223> OTHER INFORMATION: primer
198 <400> SEQUENCE: 11
199      atctatgcgg cccagccggc catg      24
201 <210> SEQ ID NO: 12
202 <211> LENGTH: 38

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Input Set : N:\Crf3\RULE60\10749522.raw.txt
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203 <212> TYPE: DNA
204 <213> ORGANISM: Artificial
205 <220> FEATURE:
206 <223> OTHER INFORMATION: primer
207 <400> SEQUENCE: 12
208     gtggtgctga gtggatccta tactacactg ccaccggg          38
210 <210> SEQ ID NO: 13
211 <211> LENGTH: 58
212 <212> TYPE: DNA
213 <213> ORGANISM: Artificial
214 <220> FEATURE:
215 <223> OTHER INFORMATION: primer
216 <400> SEQUENCE: 13
217     agctccgatg ctgaattcgg tgatagcggc tacgaagtgc atcatcagaa acctgcag      58
219 <210> SEQ ID NO: 14
220 <211> LENGTH: 52
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial
223 <220> FEATURE:
224 <223> OTHER INFORMATION: primer
225 <400> SEQUENCE: 14
226     ggtttctgat gatgcacttc gtagccgcta tcatgacgaa attcagcata gg          52
228 <210> SEQ ID NO: 15
229 <211> LENGTH: 9
230 <212> TYPE: PRT
231 <213> ORGANISM: Artificial
232 <220> FEATURE:
233 <223> OTHER INFORMATION: synthetic peptide
234 <400> SEQUENCE: 15
235     His Gln Arg Ser Ser Tyr Pro Cys Thr
236     1             5
238 <210> SEQ ID NO: 16
239 <211> LENGTH: 9
240 <212> TYPE: PRT
241 <213> ORGANISM: Artificial
242 <220> FEATURE:
243 <223> OTHER INFORMATION: synthetic peptide
244 <400> SEQUENCE: 16
245     His Gln Arg Ser Ser Tyr Pro Cys Thr
246     1             5
248 <210> SEQ ID NO: 17
249 <211> LENGTH: 9
250 <212> TYPE: PRT
251 <213> ORGANISM: Artificial
252 <220> FEATURE:
253 <223> OTHER INFORMATION: synthetic peptide
254 <400> SEQUENCE: 17
255     His Gln Arg Ser Ser Tyr Pro Phe Thr
256     1             5

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/13/2005
PATENT APPLICATION: US/10/749,522 TIME: 12:17:15

Input Set : N:\Crf3\RULE60\10749522.raw.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; N Pos. 17

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 3

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26

VARIABLE LOCATION SUMMARY
PATENT APPLICATION: US/10/749,522

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Use of n's or Xaa's(NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:10; N Pos. 17

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10749522.raw.txt

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L:187 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:189 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:190 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:10
L:190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0